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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di
                                                                                                                                                                                                                                         Score
  90.5
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                                                                                                                                                                                                     942
                                                                                                                                                                                                                                         Query
Match
  A_Geneseq_0401:*
1: /SIDS6/gcgdat
2: /SIDS6/gcgdat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                               SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1987.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1987.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1989.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1990.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1992.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1993.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1993.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1995.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1997.DAT:

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SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5
Copyright (c) 1993 - 2000 Com
                                                                                                                                                             000
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  184
442
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W23069
W71557
G14666
G14825
G14659
G14824
G14823
Y35687
W79385
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                                                                                                                                                                                                                                                                                                                                              score distribution
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                                                                                                                                                                                                                                                                                                                                                        by chance to have a the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390729
                                                      Staphylothermus ma
H. pylori GHPO 171
Helicobacter polyp
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                                                                                                       Description
                  Staphylococcus
                                   Chlamydia pneumoni
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D	W20180	18	421		79	
	Y81574	21	504		80	
Streptococcus pneu	Y81541	21	395		81	
Human PRO768 (UNQ4	B44308	21	1141		1.	
PRO768 pi	Y41752	20	1141	٠	۲.	
Integrin alpha cha	в36936	22	1137		81.5	
alpha-2k	W11804	18	487		۲.	
Human alpha 2 beta	R14149	12	487		1.	
isseria menin	Y75278	21	355			
aureus mprF pr	в11037	21	840		82	
<i>-</i>	W58862	19	474		2	
	в53159	21	378		82.5	
Recombinant high a	R80953	16	360		83	
WO9905287 Seg ID 1	W92951	20	335		83	
Hydrophobic domain	B12140	21	649		·	
Streptococcus pneu	Y81562	21	406		83.5	
Staphylococcus aur	W75788	19	363		84	
nella enteri	W88344	20	430		84.5	
ğ	W13742	16	397		84.5	
	G36490	21	284	٠	84.5	
Arabidopsis thalia	G11177	21	266		84.5	
	G11178	21	240		84.5	
Arabidopsis thalia	G11179	21	212		84.5	
H. influenzae dime	Y88627	21	279		85	
đ	Y36803	20	358		85.5	
	G50402	21	266		85.5	
is thal	G50403	21	240		•	
ţ,	G50404	21	212			
	W22180	18	473		86	
rmophi	140	18	432		. 86	
Amino acid sequenc	w	20	428		86	
idopsis thal	•	21	397		5.	
S	G14661	21	214	9.2	86.5	
ylori GHPO 7	•	19	435		8	

ALIGNMENTS

Staphylothermus

marinus esterase F1-12LC.

W23069;

17-FEB-1998

(first entry)

W23069 standard; Protein; 184

B

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pulp; pa
disease
             Callen W, Kosmotka A, Link S, Maffia AM, M Reid J, Robertson DE, Swanson RV, Warren PV;
                                                                                                                                                                                Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff.
WPI; 1997-425035/39
                                                                                                                                                               Staphylothermus marinus strain
                                                          16-FEB-1996;
                                                                                            21-AUG-1997.
                                                                                                             W09730160-A1.
                                                                                                                                       Misc-difference
                                                                           11-FEB-1997;
                                         RECOMBINANT BIOCATALYSIS INC
                                                          96US-0602359
                                                                           97WO-US02039
                                                                                                                                               Location/Qualifiers
                                                                                                                             /note= "encoded by CAG"
                         Murphy
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Staphylococcus

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RESULT W9870 FIRE SYNT W9870 W9870 W9870 W9870 W9870 W9770 W
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                                                                                                                                                                                                                                                                                              GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lighin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for
                                                                                                                                                                                                                                                                                                                                                                                    H. pylori GHPO 1719 protein
   29-JUL-1997;
                                                             01-APR-1998;
                                                                                                                                                                                                                                      Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W98870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein comprises the thermostable esterase F1-12LC of Staphylothermus marinus F1, a thermostable sulphur archaea that grows optimally at 85 deg C and pH 6.5. Newly identified polynucleotides (T79321-30) encoding claimed esterases (W23069-77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W98870 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production of highly degradable animal feeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W23088) were recovered from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and probes to identify related sequences. The esterases are stable at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19;
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laiggilivivglrnlyswsrvkgsliismgvflnligvfdevygwihflvsvlfflsii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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   97US-0902615
                                                          98WO-US06371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No. 4.4e-102;
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29-JUL-1997;
14-NOV-1996;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                   GHPO 1719;
                                                                                                                                                                                                                       09-NOV-1998
                                                                                                                                                                                                                                                                        W71557 standard; Protein; 442
                                                   14-NOV-1997;
                                                                                                      WO9821225-A1
                                                                                                                             Helicobacter pylori
                                                                                                                                                                                            Helicobacter polypeptide GHPO 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 1972-1974; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Helicobacter polynucleotides – used to develop
for the diagnosis, prevention and treatment of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Al-Garawi A, Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                     383 iimplgg---
                                                                                                                                                                                                                                                                                                                                                                                                                                          265 ftfvfeyga-nvsqgtgliftslpvvfgqm-gaigilvsilfllalafagitstvallep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211
                                                                                                                                                                                                                                                                                                                                                              154 -- IPRGAAIPELLAVFSFLPFYIR 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSWSRVKGSLIISMG----VFLNLIGVFDEVYGWIHFLVSVLFFLSIIAYFI--AISILDK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSFPLTMIALAISMSSWFNIWNNALSD-LGHAVKSSVAPIFNLGLAIGGILIVIVGLRNL
                                                                                                                                                                                                                                                                                                                                                                                                                 S-----W--IAVLLIGHIAMWYLH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN GENOME SCI INC.
MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                 infection; therapy; diagnosis; vaccine; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                    (first entry)
97US-0902615.
96US-0749051.
97US-0831309.
                                                   97WO-US21353
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97US-0881227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.6%;
22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90.5; DB 19; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller C,
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N-PSDB; V52092.
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                      G14660 standard; Protein;
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                                              Arabidopsis thaliana protein fragment SEQ ID NO: 14607.
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 termination sequence
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                                                                                                                                                                                                                             svmylteryqysrfkvtwglvalifvvgvvlifslhkdykdyltffekslfdwldfasst 382
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48; Conservative
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Pred. No. 0.01
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			fragment SEQ ID NO: 148: al transduction pathway; mapping; gene expressio
			metabolic pathway; n control; promoter;
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31-AUG-1999;
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 G14659 standard; Protein; 342 AA.
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990S-0154418

990S-0154486

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; Pred. No. 0.018;
38; Mismatches 69;
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05-MAR-1999

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07-MAY-1999;
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237-SEP-1999
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101 DEVYGWIHFLVSVLFFLS---IIAYFIAISILDKSW-IAVLLIIGHIAMWYLHFASEIPR 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 14832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G14823 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 kldygw-nmivcvamgvsqlflwarwaavsshpsnwklwvvviagglam-------
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99US-0123180

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99US-0125788

99US-0126264

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99US-0128234

99US-0130077

99US-0130510

99US-0130510

99US-0132486

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99US-0137528
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Best Local S
Matches 48
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GHAVKSSVAPIFNLGLAIGGILIVIVGLRNL---YSWSRVKGSLIISMGVFLNL--IGVF
             MSLNKHSWMDMIIFILSFSFPLTMIALA---
                                                   ch 9.5%;
1 Similarity 23.3%;
48; Conservative
                                                                                      990S-0148565

990S-0149368

990S-0149175

990S-014923

990S-014923

990S-0151086

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990S-0151086

990S-015133

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990S-0153758

990S-0154779

990S-015548

990S-015658

990S-015658

990S-015658

990S-01583

990S-015923

990S-01692

990S-01692

990S-01692

990S-0160815

990S-0160815

990S-016102

990S-016135

990S-016135
                                                    38;
                                                  Score 89.5; I
Pred. No. 0.02
8; Mismatches
                                                             DB
.027;
                                                                    21;
                                                    69;
                                                                     Length
                                                                     356;
                                                    51;
                                                   Gaps
100
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16-JUN-1999
18-JUN-1999
18-JUN

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                                                                                                                    Query Match 9.5
Best Local Similarity 22.3
Matches 42; Conservative
                                                                                                                                                                                                                                                          Y34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see X91990) of Chlamydia pneumoniae.

C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see Y34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumonia nucleotides sequences can also be used as immunogenic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥35687;
                                                                                                                                                                                                                               especially where the vector directs the expression epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae transport polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y35687 standard; Protein; 485 AA
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Page 1399-1400; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
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                                                             156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 kldygw-nmivcvamgvsqlflwarwaavsshpsnwklwvvviagglam------
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   209
                              64
                                                                                          12 IIFILSFSFPLTMIALAISMSSWF------NIWNNALSDLGHAVKSSVAPIFNLGLAI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
kgtmlvtlwafigiegavvmsgraknplsvggatvlgflgclt----iyilfsllpfgs
                        GGILIV----IVGLRNLYSWS-RVKGSLIISMGVFLNLIGVFDEVYGWIHFLVSVLFFLS 118
                                                          iinvigtifkiipliifiiltafffklavfktdfw-----ghavtkaqpslgsvssql 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVYGWIHFLVSVLFFLS---IIAYFIAISILDKSW-IAVLLIIGHIAMWYLHFASEIPR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              terldyssa-----vailgfslilailrtfdirveaarvmvsapilafvtthilyinfy 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAIPELLAVFSFLPFYIRDYFKSYT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---lleiydfppy--egyfdahs 319
                                                                                                                                                                                                   485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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97FR-0014673.
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                                                                                                                                       9.5%;
                                                                                                                         33;
                                                                                                                     Score 89.5; DB Pred. No. 0.04; Mismatches
                                                                                                                                                      DB 20;
                                                                                                                         68;
                                                                                                                                                    Length 485;
                                                                                                                         Indels
                                                                                                                                                                                                                                                of a neutralising
                                                                                                                         45;
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                                                                                                                         Gaps
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43

12 IIFILSESEPLTM------IALAISMS-SWENIWNNAL------SDLGHAVKS--- 51 vvfvv--glplslakkapghaalaalmgylmfntfinailtqwphtfganlekgvenvpg 100

32;

Mismatches

59;

Indels

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Gaps

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XX TraG P
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Query Match 9.2
Best Local Similarity 23.7
Matches 47; Conservative
                                                                                                             W79385-87 represent a Staphylococcus aureus WCHU (NCIMB 40771) protein of unknown function (W79385) and proteins that have homology with an Escherichia coli phophotransferase system II permease (W78386-87). The proteins are used to generate antibodies and to screen for antimicrobials. The products are used to treat or prevent bacterial infections, particularly where caused by S. aureus but also against Helicobacter pylori. Particular applications are to treat subjects before surgery or insertion of an in-dwelling device (alternatively the device itself is impregnated before placement). The nucleic acid sequence is used as sources of antisense sequences (for therapeutic use) or regulatory elements for controlling expression of bacterial genes, and for antibacterial screening. The protein can be also used as a vaccine.
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 69; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid from Staphylococcus aureus NCIMB 40771 - useful for, e.g. diagnosis, prevention and treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-322718/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TraG protein; Lactococcus lactis; treatment; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus protein of unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W79385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W79385 standard; Protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9823738-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterial infection; Helicobacter pylori; vaccine
                                                                                                                                                                                                                                                                                                                                                                          infection(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 tfpeifti 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 -IPELLAV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 lfqhqlanipnpstagvldilvgkwgevlmnvgliiavlsswlswtiivaeipfsaakng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US22092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0031469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "this residue is encoded by
               9.2%;
                   Score 87; DB 19; Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                 Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
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RESULT 11
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                                                                                                       Query Match
Best Local
                                                                                            Matches
                                                                                                                                                                                The present sequence is a protein (168339_1) from Staphylococcus aureus genomic DNA library. This sequence is useful in preparation of vaccines for prevention or attenuation of Staphylococcal infections (especially Saureus infections) which may cause conditions such as neonatal conjunctivitis, osteomyelitis, skin infections and toxic shock syndrome. The present sequence is also useful for detecting Staphylococcal infections in biological samples.
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                       Claim 9; Page 22; 144pp; English.
                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus polypeptide useful for preventing or attenuating a Staphylococcal infection comprises one of 32 sequences of 100-1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2000
                                                                                                                                                                                                                                                                                                                                 amino acids or their fragments -
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-237864/20.
N-PSDB; Z51236, Z512
                                                                                                                                                                                                                                                                                                                                                                                                                              Bailey CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200012678-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic shock syndrome; osteomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; antibacterial; prevention; attenuation; detection; Staphylococcal infection; neonatal conjunctivitis; skin inf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y70156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y70156 standard;
                                        290
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               97
                                                              37 IWNNALSDLGHAVKSSVAPIFNLGLAIGGILIVIVGLRNLYSWSRVKGSLIISMGVFLNL 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                   vwinais----vik-----ytlgfgvglvdyvhig-----sqingillvahntylqi 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lksiagiatldtnilggiiisaiitwihnryyskrlp--
             IGVFDEVYG -- WIHFLVSVLF --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAIPELLAVESFLPFYI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SVAPIFNLGLAI-GGILI--VIVGLRNLYSWSRVKGSLIISMGVFLNLIGVFDEVYGW 106
                                                                                                       Similarity
                                                                                                                                                            412
                                                                                                                                                                                                                                                                                                                                                                                                                              Choi GH;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0098964.
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                                                                                                       9.28;
20.78;
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                                                                                           30;
                                                                                                       Score 87; DB 21; Pred. No. 0.063;
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01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                                                                        This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHPO protein; Helicol peptic ulcer disease.
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                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 805-807; 2054pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. pylori GHPO 710 protein
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(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1998;
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                                                   107 aifvilsftkfrswvmrsipsdlravsagigafiafiglke---
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162 lgdfgdphvllgvvgiiltfalytlkirgsfiiavlitsilawvlklapypseffsmpas
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DB; X14177.
                         ------VLFFLSIIAYFIAISILDKSWIAVLLIIGHIAMWYLHFASEIPRGAAIPEL
                                                                               ILIVIVGLRNLYSW-----SRVKGSLIISMGVFLNLIGVFDEVYGWIHFLVS-----
                                                                                                                                     LTMIALAISMSSWFN-IWNNALSDLGHAVKSSVAPIFNLGL------AIGG
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                                                                                                        lsataiitilssvfnglwan--tpiamsvglglsayfsfglvqglklpwqsalgivalsg
                                                                                                                                                                                                                                                              and diagnosis
                                                                                                                                                                                                                                    435 AA;
                                                                                                                                                                  Conservative
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97US-0833457.
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990S-0134218

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l Similarity 23.9%;
48; Conservative 3
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99US-0149175

99US-0149723

99US-0149920

99US-015066

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pathway;
promoter;
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Y35302
                                                                                                                Matches
                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                           Y34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see X91990) of Chlamydia pneumoniae.

C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, crythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see Y3484-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y35302;
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Page 1119; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-357842/30
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a Chlamydia pneumoniae protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; neutralising epitope.
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  47
                       54 -APIFN-----LGLAIGGIL---IVIVGLRNLYSWSRVKG--SLIISMGVFLNLIGVFD 101
                                                                    ysmlpliifvl--
iaaifeffgalllgdrvagtiessivsvtnpmiasgdymygmtaallatgvwlqlasff- 105
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                                                                                                                Conservative
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97FR-0014673.
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                                                                                                                              9.1%;
23.1%;
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                                                      --lcgfytswnigandvanavgpsvgsgvltlrgavv 46
                                                                                                                            Score 86; DB 20;
Pred. No. 0.086;
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                                                                                                                Mismatches
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Search completed: May 30, 2001, 15:23:49 Job time: 99 sec

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Maximum Match 100%
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Perfect score:
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2: /cgn2_6/ptodata/2,

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5: /cgn2_6/ptodata/2,

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Match
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   GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd
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US-08-597-236-13
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US-08-118-270-20
US-08-18-292-480-7
US-09-097-759-4
US-09-097-759-3
US-09-097-759-3
US-08-118-270-19
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US-08-202-056-7
US-08-446-659-8
US-08-390-000A-5
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Sequence 33, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 2, Appli
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Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 3, Appli
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Sequence 5, Appli
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Sequence 19, Appli
Sequence 8, Appli
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Sequence 2, Appli
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US-08-602-359A-33 Sequence 33, Application US/08602359A Patent No. 5942430 GENERAL INCORMATION: APPLICANT: KOBERTSON, Daniel E. APPLICANT: MURPHY, Dennis APPLICANT: MURPHY, Dennis APPLICANT: MAFETA, Anthony APPLICANT: MAFETA, Anthony APPLICANT: WARREN, Patrick V. APPLICANT: USASITIESS: ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 EXECUTIVE SQUARE, STE 1400 CITY: LA JOLLA STREET: USA STREET: USA ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER PREADABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER PADRICATION NUMBER: USA ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER APPLICATION NUMBER: USA ZIP: 92037 COMPUTER APPLICATION NUMBER: USA ZIP: 92037 CURRENT APPLICATION NUMBER: USA SOFTWARE: FEBRUATION: 435 PRIOR APPLICATION NUMBER: USA ZIP: 111NG DATE: FEBRUATION: APPLICATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 39,347 REFERENCE/DOCKET NUMBER: 39010/010001 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070 INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 184 AMINO ACIDS JUNORALION OF THE SEAR MALECULE TYPE: PROTEIN US-08-602-359A-33 US-08-602-359A-33	28 75 8.0 1531 2 US-08-462-109A-4 29 75 8.0 1531 2 US-08-460-907B-2 30 75 8.0 1531 2 US-08-460-907B-4 31 75 8.0 1531 3 US-08-463-179A-2 32 75 8.0 1531 3 US-08-461-384B-2 34 75 8.0 1531 3 US-08-461-384B-4 35 75 8.0 1531 3 US-08-461-384B-4 36 74 7.9 458 1 US-08-310-271-2 37 74 7.9 458 3 US-09-292-071-27 38 74 7.9 458 3 US-09-292-071-27 40 74 7.9 458 3 US-09-292-071-29 41 74 7.9 458 4 US-09-292-069A-29 42 73.5 7.8 652 1 US-08-637-823B-32 43 73.5 7.8 652 1 US-08-582-719-2 44 73 7.7 1090 3 US-08-307-896-3
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                                                                                                                          Query Match 9.1%; Score 86; DB 1; Length 473 Best Local Similarity 24.5%; Pred. No. 0.36; Matches 52; Conservative 36; Mismatches 74; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9:
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: MOLLET, Beat
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61 LAIGGILIVIVGLRNLYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIHFLVSVLFFLSII 120
                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    NAME: Fanucci A., Allan REGISTRATION NUMBER: 30256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
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                                                              SMTKESVLTNSLVVWCFSAVFTCLGACIIYALNLSNKWYLALLLTFNLFQGGQSILSQYA 133
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----LTGALNILFLVYLPL----GITGYLM 173
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: STINGELE, Fr. APPLICANT: MOLLET, Beat
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                                                                                                                                                              134 RGIGKSKIF----AAGGVILTE-----LTGALNILFLYYLPL----GITGYLM
234 VLFFLGAGANGLLAVATKIPSIISIFNTIFTQ 265
                       154 --IPRGAAIPELLAVFSFLPFYIRDYFKSYTK 183
                                                                              174 SLVLANVGTILFFAGTLSIWKEISFKIIDKKLIWQMLYYALPLIPSSILWWLLNASSRYF 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 VLFFLGAGANGLLAVATKIPSIISIFNTIFTQ 265
                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/597,236
                                                                                                                                                                                                                                                                                       2 SLNKHSWMDMIIFILSFSFPLT----MIALAISMSS-W----FNIWNNALSDLGHAV 49
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLV----SVLFFLSIIAYF--IAISILDKSWI-----AVLLIIGHIAMWYLHFASE--
                                                                                                                     FLV-----SVLFFLSIIAYF--IAISILDKSWI-----AVLLIIGHIAMWYLHFASE-- 153
                                                                                                                                                                                                       KS-SVAPIFNLGLAIGGILIVIVGLRNLYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIH 108
                                                                                                                                                                                                                                                SMTKESVLTNSLVVWCFSAVFTCLGACIIYALNLSNKWYLALLLTFNLFQGGQSILSQYA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1155 Avenue of the Americans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                    9.1%; Score 86; DB 1; Length 473; 24.5%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LACTIC BACTERIA PRODUCING EXOPOLYSACCHARIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP 95201669.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
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                                                                                                                                 US-08-098-141-2
                                                                                                                                                       RESULT
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Best Local S
Matches 42
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                                                                                           Sequence 2, Application US/08098141 Patent No. 5441875
                  GENERAL INFORMATION:
APPLICANT: Heddiger Ph.D., Matthias A.
TITLE OF INVENTION: Urea Transporter Polypeptide
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
[NFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Haemophilus Influenzae
TITLE OF INVENTION: Dimethylsulphoxide Reductase Enzyme
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TTTY: Toronto
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                       149 TSWSFYLTVVLGGLTLSYALLIPNKQREYQLQHLPSLFAIGVSLVAIVAIYQGFNLHNIH 208
                                                                                                                                                                                                              209 SAIQNAADLVPNYAIMTVTRLCLLSIVAFLLFRVKN 244
                                                                                                                                                                                                                                                     150 FASE-----IPRGAAIPE----LLAVFSFLPFYIRD 176
                                                                                                                                                                                                                                                                                                                                111 VSVLFFLSIIAYFIAIS-----
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                                                                                                                                                                                                                                                                                                                                                                                                           ILIVIVGLRNLYSWSRVKGSLIISMG----VFLNLIG-----VFDEVY-----GWIHFL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                               HKVMFVILALLGIGFIASIMHLGLPIRAF----NSLNRVGSSMMSN-----EIAAGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSWMDMIIFILSFSFPLTMIALAISMSSWFNIWNNALSDLGHAVKSSVAPIFNLGLAIGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: Canada
M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.0%; Score 85; DB 3; Length 279; 19.4%; Pred. No. 0.24;
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Best Local Similarity
Watches 47; Conserva
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                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09046086 Patent No. 6127147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Kaplan Esq., Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: 092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/098,141
FILING DATE: 19930723
                                                                                     ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 G--HIAMWYLH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 GMFYVITWQTHLLAVACALFAAYV--GAALTNVLSVFGLPTCTWPFCI 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 -WIHELVSVLFFL------SIIAYFIAISILD------KSWIAVLLII 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 YLAATGHYNLFFPTTLLQPVSSVPNITWSEIQVPLLLRAIPVGI------GQVYGCDN 237
                               COMPUTER: IBM CONTROL OPERATING SYSTEM: SOFTWARE: FastSE(
                                                                                                                                                                                        STREET: 4000 Bell CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 -IVIVGLRNLY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 WMDMIIFILSFSFPLTMIALAISMSSWFNIWNNALSDLGHAVKSSVAPIFNLGLAIGGIL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MA
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617:227-7566
                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                               Wallis,
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                                                              IBM Compatible
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No. 6127147el Compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FASEIPRGAAIPELLAVFSF----LPFYI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SWSRVKGSLI---ISMGVFLNLIGVFDEVYG--- 105
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: CLASSIFICATION:

US/09/046,086

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US-08-118-270-20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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NAME: Falk, Stephen T
                                                  TELEPHONE: 202-628-5197
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   STREET: 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITTLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 AVLLIIGHIAMWYLHFASEIPRGAAIPELLAVFSFLPFYIRDYFKSYTKR 184
                  TELEPHONE: 202 - 1528
                                                               REFERENCE/DOCKET NUMBER: MUI
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 09-SEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 VKGSLIISMGVFLNLI----GV-FDEVYG--WIHFLVSVLFFLSIIAYFIAISILDKSWI 134
                                                                                                NAME: Townsend, Kevin REGISTRATION NUMBER: (
                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08118270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 amino acids
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Schuster, David I.
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                                                                                                                                                 UMBER: US 07/943,236
10-SEP-1992
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27.3%;
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                                                                                  MURPHY-2A
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Pred. No. 0.42;
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                                                              Matches
                                                                           Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acid
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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LENGTH: 330 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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                              25 IALAISMSSWFNIWNNALSDLGHAVKSSV-AP--IFNLGLAIGGILIVIVGLRNLYSWSR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US93/08528 FILING DATE: 09-SEP-1993
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4 IAAAITFLILFTIFGNALVIIAVLTSRSLRAPQNLFLVSIAAADILV----
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 amino acids
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                                                              Conservative
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                                                                           8.3%;
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                                                                                                                                                                                                                                                                                                                                                       34,033
                                                              17; Mismatches
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Pred. No. 1
                                                                           Score 78.5;
Pred. No. 1.
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                                                                                              DB
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                                                                                          Length 330;
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                                                              Indels
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82 VKGSLIISMGVFLNLIG--VFDEVYGWIHFLVSVLFFLSIIAYFIAISILDKSW 133

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                                                                          US-09-097-759-4
                                                                                           RESULT
GENERAL INFORMATION:
APPLICANT: Winterhalter Mr., Christopher
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                     Sequence 4, Application US/09097759A Patent No. 5972663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,085
FILING DATE: 28-AUG-1992
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ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C
STREET: 600 ATLANTIC AVENUE
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,
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                                                                                                                                                                               122 YFIAISILDKS--WIAVLLIIGH---IAMWYLHFASEI 154
                                                                                                                                                                                                                      104
                                                                                                                                             156 FFVASLILDGSATMIHSLVTIDMTTILSLMYLAFVATI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
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ZIP: 02210
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                                                                                                                                                                                                                                                                                                                             16 LSFSFPLTMIALAISMSSWFNIWNNALSDLGHAVKSSVAPIFNLGLAIGGILIVIVGLRN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                      LYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIH------FLVSVLFFLSIIA 121
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24.1%; Pred. No.
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US-09-097-759-4
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 299
TYPE: PRT
                                                                                                                                                                                                                                                    Query Match
Best Local S
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Best Local Similarity
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CURRENT FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: DE 197 26 083
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Microorganisms and Processes TITLE OF INVENTION: Preparation of L-cysteine, TITLE OF INVENTION: L-cysteine, N-acetylserine on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Microorganisms and Processes for the Fermentative TITLE OF INVENTION: Preparation of L-cysteine, TITLE OF INVENTION: L-cysteine, -acetylserine or Thiazolidine Derivatives FILE REFERENCE: Winterhalter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: DE 197 26 083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Winterhalter
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TYPE: PRT
122 YFIAISILDKS--WIAVLLIIGH---IAMWYLHFASEI 154 :|:| ||| | | | | ::: || | | :|
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                                                                                                                                                 80 INFGMPAGLASLVLQAQAFFTIMLGAFT-FGERLHGK--QLAGIALAIFGVLVLIEDSLN 136
                                                                                                                                                                                           16 LSFSSFPLTMIALAISMSSWFNIWNNALSDLGHAVKSSVAPIFNLGLAIGGILIVIVGLRN 75
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                                                                                                       LYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIH----
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FILING DATE: 1998-06-16
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                                                             -GQHVAMLGFMLTLAAAFSWACGNIFNKKIMSHSTRPAVMSLVIWSALIPIIP 188
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24.1%; Pred. No. 1.7;
tive 24; Mismatches
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TYPE: PRT
; ORGANISM: Escherichia coli
US-09-097-759-2
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Best Local Sim
Matches 38;
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Patent No. 5654417
Patent No. 5654417
GENERAL INFORMATION:
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Patent No. 5972663
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Microorganisms and Processes for the Fermentative TITLE OF INVENTION: Preparation of L-cysteine, TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives FILE REFERENCE: Winterhalter
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                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NAME: Broderick, Thomas
                                                                                                                                                                                                                                                    STREET: 1...
CTTY: Seattle
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                                                        FILING DATE:
                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      CLASSIFICATION:
                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98101-2347
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                                                                                                                                                                                                                                                                                      ADDRESSEE: Christiansen, O'Connor, Johnson, Kindness
TREET: 1420 5th Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                 LICANT: Tarr, Phillip I.
LICANT: Bilge, Sima S.
LICANT: Vary, Jr., James C.
LICANT: Vary, Jr., James C.
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38; Conservative
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                                                        14-APR-1995
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                                                                          US/08/423,564
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US-08-423-564-5
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Best Local Similarity
Matches 43; Conserv
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                                                 PRIOR APPLICATION DATA:
                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: Herewith
                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS NUMBER OF SEQUENCES: 7
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REFERENCE/DOCKET NUMBER: CF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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ATTORNEY/AGENT INFORMATION:
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CITY: Palo Alto
                                                                CLASSIFICATION:
                                                                                                                                 COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                     COUNTRY: UZIP: 94304
                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive
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                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 RNLYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIH-----FLVSVLFFLSIIAYFIAISI 128
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Corley, Neil C.
Shah, Purvi
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                                                                                                                                   FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VLLIIGHIAMWY-LHFASEIPRGAAIPELLA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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9

REFERENCE/DOCKET NUMBER:

REGISTRATION NUMBER:

36,749

PF-0345 US

Billings, Lucy J.

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US-08-194-338-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08194338 Patent No. 5474898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Venter,
APPLICANT: Fraser,
APPLICANT: McCombi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
               FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,6
                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/676,174
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 TKR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 VL-LLHDSSDYLLEACKMVNYMQYQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AMWYLHFASEIPRGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 ---YWW--YLLELGFYLSLLIRLPFDVKRKDFKEQVIHHFVAVILMTFSYSANLLRIGSL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 DEVYGWIHFLYSYLFFLS------IIAYFIAISILDKSWIAYLLIIGHI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 LFYLSSFVGGLSV------LYHESWLWAPVMCWDRYPNQTLKPSL-----
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LIBRARY: L1.

NE: 2516821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 SNR 296
                                                                                                                                              APPLICATION NUMBER: US/08/194,338 FILING DATE: 08-FEB-1994
                                                                                                                                                                                                                                                                                                                                               STREET: 620 Newport CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 21.9 nes 40; Conservative
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               COUNTRY: U:
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 IFNLGLAIGGILIVIVGLRNLY-----SWSR-----VKGSLIISMGVFLNLIGVF 100
REFERENCE/DOCKET NUMBER: NIH101.001DV1
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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         Israelsen, Ned A.

Israelsen, Ned A.

29,655
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                                                                                                                                                                                                                                                                                                                                                                  3: Knobbe, Martens, olson and Bear 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter, John C.
Fraser, Claire M.
McCombie, William R.
VENTION: OCTOPAMINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 amino acids
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21.9%; Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 179
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
186 PLVSLYRQPDGAAYPQ 201
                   147 YLHFASEIPRGAAIPE 162
                                                            127 YLALDVLFCTSSIVHLCAIS-LDRYWSVTGAVEYNLKRTPRRVKATIVAVWIISAVISFP 185
                                                                                       108 HFLVSVLFFLSIIAYFIAISILDKSW-----
                                                                                                                                                                                  Local Similarity hes 33; Conserv
                                                                                                                      67 VGNVLVVIAVLTSRALRAPQNLFLVSLASADILVATLVMPFSLANELMAYWYFGQVWCGV 126
                                                                                                                                                    63 IGGILIVIVGL-----RNLYSWSRVKGSLII-----SMGVFLNLIGVFDEVYGWI 107
                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                             ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                            internal
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24.3%; Pred. No. 3
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                                                                                                                                                                                  Mismatches
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                                                                                         -----IAVLLIIGHIAMW 146
                                                                                                                                                                                  37;
                                                                                                                                                                                 Gaps
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4.

Search completed: May 30, 2001, 15:24:03
Job time: 93 sec

Run OM protein - protein search, using sw model Scoring table: sequence: Title: Perfect score: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-382-242-33 942 May 30, 2001, 15:22:50; Search time 14.23 Seconds (without alignments) 888.617 Million cell | GenCore version Copyright (c) 1993 - 2000 MSLNKHSWMDMIIFILSFSF....AVFSFLPFYIRDYFKSYTKR 184 4.5 Compugen Ltd. Million cell updates/sec

Minimum DB Maximum DB seq length: 0 length: 2000000000 Total number of hits satisfying chosen parameters:

198801

198801 seqs, 68722935 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:*
pir2:*
pir3:* pir4:*

Database :

PIR_67:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	Ī				-	•		ω		1 1	Result No. S
i	91	91	91	91.5	92	92.5	93	93	93.5	93.5	94	94	95 .	96	96.5	97	97.5	97.5		100.5	103.5	104.5	105.5	118	126.5	129.5	142	144.5	163.5	Score
:	9.7	9.7	9.7	9.7	9.8		9.9	9.9		9.9		10.0	•	10.2	•	10.3	10.4	10.4	10.5	10.7	11.0	11.1	11.2	12.5	13.4	13.7	15.1	15.3	17.4	Query Match 1
;	643	435	313	452	407	303	487	383	870	460	510	394	1321	419	485	144	360	280	360	404	600	373	401	165	156	183	192	156	175	Length 1
	S	N	2	N	N	N	N	N	ν	N	ν	N	N	N	N	N	N	Ŋ	N	1	N	N	N	N	N	Ν	N	N	Ν	DB
4	E69373	B71850	T11272	H71706	E70309	E69585	E70480	S53379	T25338	C71884	E71695	S48522	A60165	в69819	H82822	S26026	C82445	A71694	E82442	LABECA	A82043	В75542	G82210	G72486	A75149	B71040	G71450	A71189	D75214	ΙĐ
	conserved hypothet	hypothetical prote	dehydrog		hypothetical prote	sugar transport am	probable sodium/pr	ъ			hypothetical prote	cell division cont	sodium channel pro	conserved hypothet	NADH-ubiquinone ox	ŧΩ.		hypothetical prote	probable peptide A	latent membrane pr	inner membrane cop	conserved hypothet	н	_	_	_	_	_	hypothetical prote	Description

ALIGNMENTS

RESULT D75214

hypothetical protein PAB0162 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 *sequence_revision 20-Aug-1999 *text_change 20-Jun-2000
C;Accession: D75214

R; anonymous, Genoscope submitted to the EMBL Data Library, July 1999 submitted to the EMBL Data Library, July 1999 style to the EMBL Data Library, July 1999 submitted to the EMBL Data Library, July 1999 su insights into archaeal chromosome

A; Accession: D75214 A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-175 < KAW>

A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49163.1; PID:g545 A;Experimental source: strain Orsay C;Genetics: C;Genetics: A;Gene: PAB0162
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0162

Mat	Que
Best Local Similarity 34.8%; pred. No. 8e-07; Matches 55; Conservative 28; Mismatches 64; Indels 11; Gaps 5; 24 MIALAISMSSWFNIWNALSDLGHAVKSSVAPIFNLGLAIGGILIVIVGLRNLY 77;	Query Match 17.4%; Score 163.5; DB 2; Length 175;

RESULT A71189

hypothetical protein PH1785 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000 C;Accession: A71189

R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: A71189

A; Molecule type: DNA A; Status: preliminary; nucleic acid sequence not shown; translation not shown

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C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000 C;Date: 1671450 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamo M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushid
                                         hypothetical protein PH1610 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 C;Accession: B71040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-156 <KAW>
A;Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30904.1; PID:g3258221
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by C;Genetics:
A;Gene: PH1785
       R;Kawarabayasi, n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29334.1; PID:g3256651 A;Experimental source: strain OT3 A;Note: this accession replaces an interim accession for a sequence replaced C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogucr DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
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C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0162
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C;Species: Pyrococcus horikoshii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 LDKSWIAVLLIIGHIAMWYLHFASEIPRGAAIPELLAVFSFLPFYI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 VIVGLRNLYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIHFLVSVLFFLSIIAYFIAISI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 IIFILSESEPLTMIALAISMSSWENIWNNALSDLGHAVKSSVAPIENL---GLAIGGILI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                          IIG-HIAMWYLHFASEIPRGAAIPELLAVFSFL 170
                                                                                                                                                                                                                                                                                                                                                                      WFNIWNNALSDLGHAVKSSVAPIFNLGLAIGGILIVIVGLRNLYSW----SRVKGSLIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSRTWRITATITETIMVILVSFKI----GLAIPELIGAAAILSYIL 150
                                                                                                                                                                                         LLGVPLALWSL----KKFEGVAVAETISIVVFL 182
                                                                                                                                                                                                                                                                                                MG-VFLNLIGVFDEVYGWIHFLVSVLFFLSIIAYFIAISILDKSWI-----AVLL 138
                                                                                                                                                                                                                                                                                                                                    WWGITENAISDLGR-IGLPYNWVMNISLILGSVCLIIYG----AWRFKKSKDIGWLLYM 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVMVIYF --- IIGLALVISQNPWFSFTKNALSDMGSA-KNPKGWMFNLYIIGLGIIGIIV
                                                                                                                                                                                                                                                              LGSVFLGLIGIFPEGTN-LHYEVSWGFFVSM---FLAILLLSISFLIRGNKLGIVGLMLF
                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
       Y.; Sawada,
; Funahashi,
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                          #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                           15.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LKISM-ILLILVGIFPEEEP-PHTPSAILMYL---LSFIDMGL
                                                                                                                                                                                                                                                                                                                                                                                                            32;
     Horikawa, H.; Haikawa,
Tanaka, T.; Kudoh, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 144.5; DB 2;
Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 142; DB 2;
Pred. No. 5.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 192
     Y.; Hino, Y.;
Yamazaki, J.;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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     Yamamoto,
Kushida, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto,
Kushida,
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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     N.;
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Oguchi
     Oguchi
                      Sekin
G72486
hypothetical protein
C; Species: Aeropyrum
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                                                                                                                                                                                       Вb
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A75149
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                                                          RESULT
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A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30722.1; PID:g3258039
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
"~+~hes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain C; Genetics: A; Gene: PAB0225
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-156 <KAW>
A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A; Description: Pyrococcus abyssi genome sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
C;Accession: A75149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Gene: PH1510
C:Superfamily: Pyrococcus abyssi hypothetical protein PAB0162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 5, 55-76, 1998
A;Title: Complete sequence a
A;Reference number: A71000;
A;Accession: B71040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A75149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PAB0225 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-183 <K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 ILALLGLFIPWPSVAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 FIAISILDKSWIAVLL 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 VKGSLIISMGVFLNLIGVFD------EVYGWIHFLVSVLFF------LSIIAY 122
                                                                                                                                 72 GLRNLYSWSRVKGSLIISMGVFLNLIGVFDE---VYGWIHFLVSVLFFLSIIAYFIAISI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 SISNNPWFSFFKNALSDLGDPAKASHPWIYNYGLIVTSPFVLAFSIYLIIAAKN--KIQT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 AISMSSWFNIWNNALSDLGHAVKSSVAPIFNLGLAIGGILI-----VIVGLRNLYSWSR 81
                                                                                                                                                                                4 ALSIALTLYFILGLALVVHENSWFSFSKNALSDMG-SLRNPKGWMFN-----VFIIGL
                                                                                                                                                                                                                 SESEPLTM-----IALAISMSSWENIWNNALSDLGHAVKSSVAPIFNLGLAIGGILIVIV 71
                                          LDKSWIAVLLIIGHIAMWYLHFASEIPRGAAIPELLAVFSFLPFYI 174
                                                                                      GLLGLVTSLMLKRKILTLSMAFLVLVGVFPEEKPLHTPSAILTYILAFTDMVIYG-----
-GIWRVVGIGTFMVMLFLINLKVGLAIPELIGAASILAYIL
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                          13.4%; Score 126.5; DB 25.3%; Pred. No. 0.00082;
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Pred. No. 0.00054;
2; Mismatches 47
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                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                       64;
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APE2535

Aeropyrum

pernix

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A;RCTESSACIA.
A;RCTESSACIA.
A;RSTATUS: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <HEI>
A;Residues: 1-401 <HEI>
A;CTOSS-TEFERENCES: GB:AE004215; GB:AE003852; NID:g9655842; PIDN:AAF94519.1; GSPDB:GN001
A;CTOSS-TEFERENCES: GB:AE004215; GB:AE003852; NID:g9655842; PIDN:AAF94519.1; GSPDB:GN001
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A;Molecule type: DNA
A;Residues: 1-165 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaiawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; l DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy. A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                        A; Gene
A; Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid ABC transporter, permease protein VC1361 [imported] - Vibrio cholerae (group C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C;Accession: G82210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolæeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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  135 YIETFRNL-PLLLQIFFWYFVVLQALPSARESMHLGEWFYLNIKGLYLAKPIFESGSIWV 193
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                                           SMGVFLNLIGVFDEVYGWIHFLVSVL------FFLSIIAYFIAISILDKS--WI 134
                                                                                                                                                                          HSKHTNLLYNPTFRSVVFQLLAVCVLAFFLYTIVNNALTNLESRGIATGFAFLEQTAGFG
                                                                                                                                                                                                                   HSWMDMIIFILSF-SFPLTMIALAISMSSWFNIWNNALSDL--
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                                                                                      ISQSLIPYDETYSYGRTFLVGLLNTALVSVLGILLATILGFLIGIARLSSNWLISRLAAV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                           11.2%; Score 105.5; 1
20.1%; Pred. No. 0.1;
tive 38; Mismatches
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Pred. No. 0.0043;
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                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                                                                84;
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                                                                                                                                                                                                                                                                                                         Length 401;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                61;
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Query Match
Best Local Similarity
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inner membrane copper tolerance protein cyc2 VC2701 [similarity] - Vibrio cholerae
N;Alternate names: thiol:disulfide interchange protein DsbD
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75542
                                                                                                  A; Molecule type: DNA
A; Residues: 1-600 <HEI>
A; Cross-references: GB: AE004336;
                                                                                                                                                                                                                A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: A82043
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C; Superfamily: Bacillus subtilis conserved hypothetical protein
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A;Experimental source: strain R1
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A; Residues: 1-373 <WHI>
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A; Accession: B75542
                                              C; Genetics:
                                                                                                                                                                                                                                                                                                   1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                        R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: DR0252
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A;Map
                                                                           A; Experimental source: serogroup
                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: A82043
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Best Local
position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 SMSSWF-NIWNNALSDLGHAVKSSVAPIFNLGLAIGGI-----LIVIVGLRNLYSWSRVK 83
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43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                           GB:AE003852; NID:g9657296; O1; strain N16961; biotype
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Pred. No. 0.12;
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                                                                              PIDN:AAF95841.1;
El Tor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
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*11.0%; 22.5%;

Score 103.5; DB Pred. No. 0.22;

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Length 600;

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RESULT
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   probable peptide ABC transporter, permease protein VCA0590 [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hu, L.F.; Zabarovsky, E.R.; Chen, F.; Cao, S.L.; Ernberg, I.; Klein, G.; Winberg, G. J. Gen. Virol. 72, 2399-2409, 1991
A;Title: Isolation and sequencing of the Epstein-Barr virus BNLF-1 gene (LMP1) from a A;Reference number: JQ1434; MUID:92013956
A;Accession: JQ1434
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A;Note: the authors translated the codon AAA for residue 358 as Ala
A;Note: warning: the organism was shown incorrectly as Homo sapiens in GenBank accession
C;Comment: Unlike Epstein-Barr nuclear antigen 1 (EBNA-1) (see PIR:S42440), which is exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992
C;Accession: JQ1434; G00065; S21660
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A; Residues: 1-404 <H
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#sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                         -VSVLFFLSIIAYFIAISILDKSWIAV-----LLIIGHIAMW-YLH 149
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Pred. No. 0.27;
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C;Geneti
A;Gene:
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein RP368 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 2
C;Superfamily: oligopeptide permease protein oppB
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                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14827.1; PID:g386
A;Experimental source: strain Madrid E
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The genome sequence of Rickettsia prowazekii A;Reference number: A71630; MUID:99039499 A;Accession: A71694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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A; Residues: 1-360 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-280 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: VCA0590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown; translation not
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Best Local
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 VSISLGLWSTLLIYLI--SIPLG-ISKAIHHGSRFDVWSSAVVIIGYAIP-
230 LKEIFACFIGILFYFISLSIL
                                                                                          174 LGLSISNGLAALTGTLS----AQVNGFADINMGYGVALVGIGAIIIGRQIFLNNINNFNA 229
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                                         114 ---LF--FLSIIAYFIAISIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LAIGGILIVIVGLRNLYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIHFLVSVLFFLSII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
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                                                                                                                                                                                                                                3 LNKHSWMDMIIFILSFSFPLTMIALAISMSSW---FNIWNNALSDLGHAVKSSVAPIFN-
                                                                                                                                                                                                                                                                                                                                                                                                   RP368
                                                                                                                                                                                      LDLDNWLVPLILINSFIIVIVLILLKGNLGLFLRAFGFNKDLLIDLG-----KPAELYRM 173
                                                                                                                                        LGLAIGGILIVIVGLRNLYSWSRVKGSLIISMGVFLNLIGVFDEVYGWIHFLVSV-----
                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                    10.4%; Score 97.5; DB 2; 27.7%; Pred. No. 0.34;
                                           129
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Pred. No. 0.36;
29; Mismatches
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El Tor
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H.; Dragoi,
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hypothetical protein VCA0550 [imported] - Vibrio cholerae (group Ol strain N16961) C; Species: Vibrio cholerae (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000 C;Accession: C82445 R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-144 <OKI>
A; Cross-references: EMBL: X54252; NID: g13988; PID: g2654243
A; Cross-references: EMBL: X54252; NID: g13988; PID: g2654243
A; Cross-references: EMBL: X54252; NID: g13988; PID: g2654243
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A;Title: The mitochondrial genomes of two nematodes, Caenorhabditis elegans and A;Reference number: S26014; MUID:92201635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Caenorhabditis elegans mitochondx (;Species: mitochondrion Caenorhabditis elegans C;Decies: n=reb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Jun-2000 C;Accession: S26026; S25799
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                                                                                                             A;Start codon: ATA
C;Superfamily: NADH dehydrogenase (ubiquinone) chain
C;Keywords: mitochondrion; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                            R;Okimoto, R.; Macfarlane, J.L.; Wolstenholme, Nucleic Acids Res. 18, 6113-6118, 1918, 1918, A;Tille: Bvidence for the frequent use of TTG A;Reference number: S13139; MUID:91045077
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A; Residues: 1-360 <HEI>
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A;Status: preliminary
                                                                                                                                                                                                                                                         A;Genetics:
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-25 < OK2>
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                                                                                                                                                                                                                                 A; Genome: mitochondrion
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Best Local Similarity
Matches 45; Conserv
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 W-----IHFL-----VSVLFFLSIIAYFIAI-----SILDKSWIAVLLIIG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WQDVVISIMGPCFGFLLSLLLVGVYWVTDSPFWAALAVFNAFLNLFNLLPVLPLDGGHIL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMDMIIFILS--FSFPLTMIALAI----SMSSW-----FNIWNNALS------DLGHAV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WRQRHHSHLLPLNRYAQMVSTIWYFALVSGLIAIIIGFASTGDTLLSLPLLLILG
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10.3%;
Score 97; DB 2
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       as the translation initiation codon
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                       2;
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                             Length 144;
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Search completed: May Job time: 91 sec

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submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A;Reference number: A59328
                                                                                                              В
                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 bel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
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Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADH-ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE003884; GB:AE003849; NID:g9105127; PIDN:AAF83129.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-485 <SIM>
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Best Local
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                                                    131 KSWIAVLLIIGHIAMWYLHFASEIPRGAAIPELLAVFSF 169
                                                                                                                                                                                                                                                                                          15 ILSFSFPLTMIALAISMSSWFNIWNNALS--DLGHAVKSSVAPIFNLGLAIGGILIVIVG 72
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                                                                                                                                                                                                                                      22 LLGSTFALLMIDLFIGQAR--KVWTHFLSVAILGVVLSMLVAGVGGQGAAFHGMF-----
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                                                                                                                 VRDSAADVMKVVIVLVSALSLVYGWSYLRERNLFQGEIPVLVLFATLGMM- 124
                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 96.5; DB 25.8%; Pred. No. 0.68;
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NU6M_CAEEL
YHAP_BACSU
UT2_RAT
ALA5_ARATH
CC91_YEAST
A2AB_RAT
A2AB_MOUSE
ARCD_LACSK
ALAA_ARATH
CCX3_GADMO
FLIR_ERWCA
YIDE_HAEIN
COP_CLOPE
YVBV_BACSU
YEJB_ECOLI
TAGG_BACSU
Y440_METJA
Y189_MYCPN
NUJM_CROYA
NULM_CROYA
COX1_BACSU
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ATP6_APILI
Y23B_MYCPN
Y233_METJA
UT2_HUMAN
NU1M_RHISA
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P42946
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007523 bacillus su
Q62668 rattus norv
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   P24010
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54 APIFNLGLAIGGILIVIVGLRNLYSWSRVKGSLIISMGVFLNLIGVFDEVYG-WIHFL-- 110 LSSSIGLALLLLLLALLFWLYI---VMSDWTGGALLVLYSFALMLIIILIIFIFRRDLL Query Match 10.7 Best Local Similarity 23.6 Matches 42; Conservative

10.7%;

28;

Score 100.5; Pred. No. 1.1; 28; Mismatches

DB 1; 53;

Length 404; Indels

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LSFSFPLTMIALAISMSSWFNIWNNALSD-LGHAV--

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Gaps

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                                                                                                                                                                                                                                                                                      Hypothetical protein;
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Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.; "The mitochondrial genomes of two nematodes, Caenorhabditis elegans and Ascaris suum."; Genetics 130:471-498(1992).
Noback M.A., Terpstra P., Holsappel S., Venema G., Bron Submilted (JUN-1997) to the EMBL/GenBank/DDBJ databases -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PO-i- SIMILARITY: TO M.JANNASCHII MJ1024.
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NADH-UBIQUINONE OXIDOREDUÇTASE CHAIN 6 (EC 1.6.5.3).
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Bacteria; Firmicutes;
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                   -i- FUNCTION: SPECIALIZED LOW-AFFINITY UREA TRANSPORTER. MEDIATES TRANSPORT IN KIDNEY.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                       "Molecular cloning and characterization of the vasopressin-regulated urea transporter of rat kidney collecting ducts.";
J. Clin. Invest. 98:2580-2587(1996).
                                                                                                   STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney inner medulla. MEDLINE-97117152; PubMed-8958221;
                                                                                                                                                                   "Cloning and regulation of expression
                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney; MEDLINE-95386714; PubMed-7657826;
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                 Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.F., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujli C.Y., Gildsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE 5
                                                                                                                                                                                            STRAIN=CV. COLUMBIA; MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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  Kurtz D.B.,
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SEQUENCE
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                       -VSVLFFLSII----AYFIAISILDKSWIAVLLIIGHIAMWYLHFASEIPRGAAIPELLAV
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PHOSPHORYLATION (BY SIMILARITY).
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Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Favello A., Fulton L., Gáttung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Pell Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Rifken L., Wohldman P., Vaudin M., Wilson R., Waterston R. Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.
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01-NOV-1995 (Rel. 32, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
CELL DIVISION CONTROL PROTEIN 91.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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MEDLINE=99120557; PubMed=9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D.,

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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EMBL; Z49383; CAA89402.1;
SGD; S0003644; YJL108C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A 37.5 kb region of yeast chromosome X i and CSD3 genes, a TCP-1-related gene, an to the DALBO gene, and a tRNA(Arg)."; Yeast 11:873-883(1995).
           HYPOTHETICAL
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MEDLINE=96090136; PubMed=7483851;
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          30, Created)
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KDA PROTEIN IN MFD-DIVIC
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"Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
SIMILARITY: STRONG, TO B.SUBTILIS SPOVB.
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35; Mismatches
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SEQUENCE
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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STRAIN-26695 / AFCC 700392;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.,
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pylori.";
Nature 388:539-547(1997).
Nature 388:539-547(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Helicobacter.
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01-APR-1993 (1
30-MAY-2000 (1
ATP_SYNTHASE 1
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PRINTS; PRO0123; ATPASEA.

PROSITE; PS00449; ATPASE_A; 1.

Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.

Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization."; Genetics 133:97-117(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crozier R.H., Crozier Y.C.;
"The cytochrome b and ATPase genes
Mol. Biol. Evol. 9:474-482(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP6.
Y23B_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L06178; AAB96802.1; -. EMBL; M87065; AAA31634.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crozier R.H., Crozier Y.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93114603; PubMed=8417993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92261310; PubMed=1533894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apis mellifera ligustica (Common
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoidea; Apidae; Apis.
                                                                                                                                                137
                                                                                 187
                                                                                                                                                                             53
                                                                                                                                                                                                             77
                                                                                                                                                                                                                                              1 MSLNKHSWMDMIIFILSFSFPLT---MIALAISMSSWFN----IWNNALSDLGHAVKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE. SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL;
                                                                                 SILPINLMIQNMLLTLEIFMSMIQSYVFSILLIL
                                                                                                                HFL-VSVLFFLSIIAYFIAISILDKSWIAVLLII 140
                                                                                                                                                                           VAPIFNLGLAIGGILIVIVGLRNLY--SWS---RVKGSLIISMGVFLNLIGVFDEVYGWI 107
                                                                                                                                                                                                             ISLMLYIMITNIFSLIPYVFTLTSHLLLNMILSLTLWFSFLIYLIYNNYIMFLSHLVPLN 136
                                                                                                                                              -SPVFLMN-----FMVITELISLITRPWTLSTRLSANL-ISGHLILTLLGIF--ISNFI 186
                                                                                                                                                                                                                                                                                                                                                                                                                         PF00119; ATP-synt_A; 1.
                                                                                                                                                                                                                                                                                               Similarity
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(Rel.
(Rel.
E A CHA
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el. 25, Last sequence update)
el. 39, Last annotation update)
el. 39, Last annotation (PROTEIN 6).
 STANDARD;
                                                                                                                                                                                                                                                                                             9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endopterygota; Hymenoptera; Apocrita; Aculeata;
                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                               Score 89;
Pred. No.
   PRT;
                                                                                                                                                                                                                                                                                Mismatches
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 243
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                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                             DB 1;
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 A
                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                             Length 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IT MAY PLAY
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Best Local Similarity
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                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
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Y233_METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=ATCC 29342 / M129; MEDLINE=97105885; PubMed=8948633;
SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L.,
                                                                                                                                  HYPOTHETICAL
                                                                                                                                                                                     Q57685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MG323.1 HOMOLOG (P01_ORE243).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P75314;
30-MAY-2000
                                                                              Methanococcus
                                                                                          Archaea; Euryarchaeota;
                                                                                                         Methanococcus jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPN469 OR MP372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Complete sequence
                                                                                                                                                                                                                                                                 142 GFYFSVVAYCF-----WIALMLL
                                                                                                                                                                                                                                                                                        114 LFFLSIIAYFIAISILDKSWIAVLLI 139
                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                                                                              13 IFILSFSFPLTMIALAI------SMSSWFNIWNNALSDLGHAVKSSVAPIFNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE000035; AAB96020.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                   PROTEIN MJ0233.
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99
                                                                                                                                                                                                                                                                                                                                           -GILIVIVGLRNLYSWSRVKGSLIISMGVFLNLIGVF--DEVYGWIHFLVSV
                                                                                                                                                                                                  STANDARD;
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119
163
224
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                                                                                                                                                                                                                                                                                                                                                                                                                                    9.48;
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                                                                                            Methanococcales; Methanococcaceae;
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POTENTIAL.
POTENTIAL.
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Pred. No. 4.5;
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DFD7355C3DD876FE CRC64;
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                                                                                                                                                         update)
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                                                                                                                                             update)
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    Fleischmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 243;
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Best Local Similarity
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01-NOV-1997 (Rel. 35, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation updat
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                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                    SLC14A2 OR UT2 OR HUT2.
                                                                                                                                                                                                                         UREA TRANSPORTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of jannaschii."; Science 273:1058-1073(1996).
MEDLINE=96228053; PubMed=8647271;
Olives B., Sonia M., Mattei M.-G.,
                                                  TISSUE-Kidney
                                                                                                           NCBI_TaxID-9606;
                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U67479; AAB98226.1; TIGR; MJ0233; -.
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LPLNIIDIFISYS 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIISVISLWLYSKLAEVNYSVKGFYGFFEFKEIFKMIGIRYIILVIIIAIINFIISLIVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIMHIIMSFLIYFGIIFIIGLIVSAIIGGYNVRIMKTTVEGLNVAPDWNNITDLLYRGIL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I protein;
23 43
61 83
117 13;
114 16;
197 21
221 24
243 26
277 AA; 3
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31306
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81
137
164
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Primates;
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3 POTENTIAL.
1 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
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- FUNCTION: SPECIALIZED LOW-AFFINITY UREA TRANSPORTER.

- TRANSPORT IN KIDNEY.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

- TISSUE SPECIFICITY: KIDNEY.

- SIMILARITY: TO OTHER MAMMALIAN UREA TRANSPORTERS.
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"Molecular characterization of a new urea transporter in
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GMFYVITWQTHLLAIACALFAAYL--GAALANMLSVFGLPP
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48; Conserv
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29; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9.6	9.6	9.6	9.6	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.8	9.8	9.8	9.9	9.9	9.9	9.9	10.0	10.0	10.0	10.1	10.1	10.1
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ALIGNMENTS

Qy 78 S Db 69 K Qy 136 V Db 128 F	Query Match Best Local: Matches 5 Qy 24 MIA Db 10 IIA	OC Archaea; E OX NCBI_TaxID RN [1] RP SEQUENCE F RC STRAIN-ORS RA Heilig R.; RT "Pyrococcu RT structure RT Structure RL Submitted DR EMBL; AJ24 KW Hypothetic SQ SEQUENCE	SUL V23
SWSRVKGSLIISMGVFLNLIGVFDEVYGWIHFLVSVLFFLSIIAYFIAISILDKSWIA 135 :::	Query Match 17.4%; Score 163.5; DB 1; Length 175; Best Local Similarity 34.8%; Pred. No. 0.00013; Matches 55; Conservative 28; Mismatches 64; Indels 11; Gaps 24 MIALAISMSSWENIWNNALSDLGHAVKSSVAPIENLGLAIGGILIVIVGLRNLY 77	Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus. Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus. SEQUENCE FROM N.A. STRAIN-ORSAY; Heilig R; Heilig R; "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ catabases. EMBL; AJ748283; CAB49163.1; Hypothetical protein. Hypothetical protein. Hypothetical protein. 175 AA; 19133 MW; 19AB460C3DC15f79 CRC64;	T 1 Q9V235 PRELIMINARY; PRT; 175 AA. Q9V235; Q9V235; PRELIMINARY; PRT; 175 AA. Q9V235; PRELIMINARY; PRT; 175 AA. Q1-MAY-2000 (TrEMBLrel. 13, Created) Q1-MAY-2000 (TrEMBLrel. 14, Last sequence update) HYPOTHETICAL 19.1 KDA PROTEIN. PRESCOCCUS ANGRES

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                                                 "Complete sequence and gene organization thermophilic archaebacterium, Pyrococcus DNA Res. 5:55-76(1998).
                               EMBL;
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                                                                                                                         Shizuya H., Kikuchi H.
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L 17.5 KDA PROTEIN PH1785.
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                            BAA29334.1;
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Pred. No. 0.0025;
30; Mismatches 59;
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                                                                        of the genome of a hyper-
horikoshii OT3.";
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01-MAY-2000
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Hypothetical |
SEQUENCE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  059239;
                                        Q9V1S7
                                                                                                                                                                                                                                                                                                                                              Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Ni Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Offul Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Og Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K. Masuchi Y., Shizuya H., Kikuchi H., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a h: "bermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
EMBL, APO00006; BAA30722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 20.6 KDA PROTEIN PH1610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota;
NCBI_TaxID=53953;
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les 40; Conserv
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Last sequence update)
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Pred. No. 0.0044;
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horikoshii OT3.";
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                                                                                                                                                                                                                                                                               "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1.";
DNA Res. 6:83-101(1999).
EMBL; AP000064; BAA81551.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y8U9 PRELIMINARY; PRT;
Q9Y8U9; PRELIMINARY; PRT;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pyrococcus abyssi genome sequence: insights into archaustructure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ248284; CAB49272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
                                                                                                                                                                                                                                 Hypothetical SEQUENCE 16
                                                                                                                                                                                                                                                                                                                                                                                     Yamazaki J., Kushida N., Oguchi A., Aoki K.,
Nomura N., Sako Y., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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HYPOTHETICAL 17.2 KDA P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99310339; PubMed=10382966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aeropyrum pernix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLLGLVTSLMLKRKILTLSMAFLVLVGVFPEEKPLHTPSAILTYILAFTDMVIYG-----
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SDWFVFTEHAFSDLG-GVKARMPWIYNYGLILVGLLVTLYSLCPYRAAVERLEAFGSGLL
                                                SSWFNIWNNALSDLGHAVKSSVAPIFNLGLAIGGILIVIVGL---RNLYSWSRVKGS-LI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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165 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 13, Last annotation update) 18.1 KDA PROTEIN APE2535.
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                                                                                                                                                                                                                                 18081 MW;
                                                                                                12.5%; Score 118; DB 30.4%; Pred. No. 0.18; tive 20; Mismatches
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3; Mismatches
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                                                                                                                                                                                                                                 82E9EC27C6669C15 CRC64;
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                                                                                                                                                1;
                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                               Kubota K., Nakamura
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                                                                                                   22;
                                                                                                   Gaps
  61
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01-CCT-2000 (TrEMBLrel. 15, L
01-CCT-2000 (TrEMBLrel. 15, L
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation updat
CYTCCHROME C OXIDASE SUBUNIT 1.
SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
                                                  Bacteria; Proteobacteria;
NCBI_TaxID=666;
                                                                                                                                                                           Q9KS98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPRO00883; -. PFAM; PF00115; COX1; 1. PRINTS; PR01165; CYCOXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF087002; AAF13732.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                    148 LHFASEIPR----GAAIPELLAVFSFLPFYI 174
                                                                                                                                                                                                                                                                                              140 VAGAY--LWGWTAVGAAIEILFQILPVAVGLKTTIDAGLARVFFSWTLHAIVYFWLIPAY
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                                                                                                                                                                                                                                                                                                                        96 LIGVFDEVYGW--IHFLVSVLFFLSIIAYFIAISI-----LDKSWIAVLLIIGHIAMWY 147
                                                                                                                                                                                                                                                                                                                                                                                                        27
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                                                                                                                                                                                                                                                                                                                                                   GLSSVLYTFYPPMIGSPFYYLGVVLVVVGSWIWVALMSVNLYAWKKRNPGTPIPLAMFAN
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A; 56155 MW;
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                                                                 gamma subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109.5;
Pred. No. 1.9;
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                                                                  Vibrionaceae;
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                                                                                                                                                                  TIGK; INTERPRO; I. INTERPRO; I. INTERPRO ; II. INTERPRO ; III. INTERPRO ; II. INTERPRO ; III. INTERPRO ; II. INTERPRO ; III. INTERPRO ; II. INTERPRO ; III. INTERPRO ; II. 
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                                                                                                                                                                                                                                                                                                                              radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001886; AAF09838.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J. Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L Dodson R.J., Haft D.H., Jang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C. Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
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EMBL; AE004215; AAF94519.1;
TIGR; VC1361; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                             "Genome Sequence of the Radioresistant Bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIETFRNL-PLLLQIFFWYFVVLQALPSARESMHLGEWFYLNIKGLYLAKPIFESGSIWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMGVFLNLIGVFDEVYGWIHFLVSVL------FFLSIIAYFIAISILDKS--WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSKHTNLLYNPTFRSVVFQLLAVCVLAFFLYTIVNNALTNLESRGIATGFAFLEQTAGFG
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   43;
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                                         Similarity
                                                                                                                                                                                                                                                             IPR002549;
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   Conservative
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                                                                                                                                                                                                                       UPF0118; 1.
                                                                                                                                                                                  40283 MW;
                                     11.18;
27.48;
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20.1%;
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   29;
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                                     Pred. No. 3
                                                                       Score 104.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ASEIPRGAAIPELLAVFSFLPFYI 174
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                                                                                                                                                                                     502D3FE29051E6F7
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   Mismatches
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M., Shen M.,
Zalewski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.,
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41;
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RESULT 11
Q9VGYO
ID Q9VGYO
AC Q9VGYO
DT 01-MAY
DT 01-JUN
DE CG4073
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Best Local ?
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01-MAY-2000 (TrE
01-JUN-2000 (TrE
CG4073 PROTEIN.
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01-OCT-2000
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STRAIN-EL TOR N19961 / SEROTYPE 01;

MEDLINB=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M. Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Selle McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter Fraser C.M.;
                                                                                                                             Q9VGY0
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TIGR;
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                              (TrEMBLrel.
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PROTEIN DSBD.
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Pred. No. 5.5;
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                           update)
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Best Local
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EMBL; AE003688; AAF54542.1; "
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Amanatides P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLYBASE; FBgn0037827; CG4073.
SEQUENCE 293 AA; 32710 MW;
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226 MRYVSMVSLIYVASLILFTI
                                        155 PRGAAIPELLAVFSFLPFYI 174
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                                                                                                                              NLIGVFDEVYGWIHFLVSVLFFLSIIAYFIAISILDKSWIAVLLIIGHIAMWYLHFASEI 154
                                                                                                                                                                                                                                                           KHLGWVYLIHAVLSASAVIQLVVLRL------CNKDFGELISPSVPSFVWLLLAV 121
                                                                                                                                                                       GCVLIMAYVYLANQCPCNGLLAIVIVEVIVIFVNCHRWARLSMLWMTGVLSLVLALNVML
                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                      -VYLPLKILPGSIFM - - IVLTFCCIAIV - - -
                                                                                                                                                                                                                                                                                                                                                                   10.9%;
                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                               Score 102.5;
Pred. No. 3.5;
82; Mismatches
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Hoskins R.A.,
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                                                                                      -VSIYLIV--
                                                                                                                                                                                                                                                                                                                                                 62;
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RESULT 13
Q9KLZ9
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01-NOV-1999
01-NOV-1999
01-MAY-2000
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01-0CT-2000
01-0CT-2000
                                                                                     SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

STRAIN-20466833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A.,

Heidelberg J.F., Eisen J.A., Potential To Hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burger G., :
Lang B.F.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.
                                                                                                                                                                                                                                                                Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                           Q9KLZ9;
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PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome of Tetrahymena pyriformis.
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"Expression of mitochondrial protein-coding genes
pyriformis.";
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Tetrahymenina; Tetrah;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion
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                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
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                                                                                                                                                                                                                 NCBI_TaxID=666;
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37; Conserv
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                                                                                                                                                                                                                                                                                                            15, Created)
15, Last sequence update)
15, Last annotation update)
, PERMEASE PROTEIN, PUTATIVE
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                                                                                                                                                                                                                                          gamma subdivision; Vibrionaceae; Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101.5; |
Pred. No. 4.9;
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comparison
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                                                                                                 Gwinn M.L.,
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Best Local Similarity
Matches 53; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Wilding C.S., Mill P.J., Grahame J.;

Wilding C.S., Mill P.J., Grahame J.;

"Partial sequence of the mitochondrial genome of Littori

relevance to gastropod phylogenetics.";

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MADIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS 1
                                                                                                                                                                                                                                                                                            PFAM: PF00119; ATP-Synt_A; 1.
PRINTS: PR00123; ATPASEA.
PROSTIE: PS00449; ATPASEA; 1.
Mitochondrion; Hydrogen ion transport; CF(0); Transmeml SEQUENCE 231 AA; 25478 MW; 7EEAF487BC53A67A CRC64;
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Q9ZZU5;
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000).

Nature 406:477-483(2000).

EMBL; AE004389; AAF96492.1; -.

TIGR; VCA0590; -.

SEQUENCE 360 AA; 40400 MW;
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Fraser C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) ATP SYNTHASE A CHAIN (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Cae
Neotaenioglossa; Littorinoidea; Littorinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholerae
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EMBL; AJ132137; CAA10596.1;
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NCBI_TaxID=31220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 VSISLGLWSTLLIYLI--SIPLG-ISKAIHHGSRFDVWSSAVVIIGYAIP--
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60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIRECT NAME ...

(BY SIMILARITY).

(BY SIMILARITY).

SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1).

CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSII HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).

HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
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                                                                                                      SLNKHSWMDMIIFILSFSFPLTMIALAISMSSWFN--IWNNALSDLGHAVKSSVAPIFNL
                                                      SFDDNNQVFMSLYMLMWAFSLVII-LIFSSSYWVTGPRWAPIISLFKDTISSQVFRSF--
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                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%;
                                                                                                                                                            10.4%; Score 97.5; D
24.2%; Pred. No. 6.2;
tive 34; Mismatches
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Pred. No. 7
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dae; Littorina.
                                                                                                                                                                                                                  DB 8;
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01-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., W Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein SEQUENCE 360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDIINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCA0550.
Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
EMBL; AE004386; AAF96452.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rigr; vcA0550;
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                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 45; Conserv
                                                                                                                                                                                                                                                                 8 WMDMIIFILS--FSFPLTMIALAI----SMSSW-----FNIWNNALS------DLGHAV 49
                                                   W-----IHFL-----VSVLFFLSIIAYFIAI-----SILDKSWIAVLLIIG
WRQRHHSHLLPLNRYAQMVSTIWYFALVSGLIAIIIGFASTGDTLLSLPLLILG
                                                                                                             KS---VSFSMNSKMGVILCVLAILGGI-----ALSYSLGLTLFGFLLLMGALDIVFE
                                                                                                                                                                      KSSVAPIFNLGLAIGGILIVIVGLRNLYSWSRVKGSLIISMGV----FLNLIGVFDEVYG
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(TremBLrel. 15, Last sequence update)
(TremBLrel. 15, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                           Score 97.5;
Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                          DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 360;
                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sellers P.,
                                                      141
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                      105
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